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POLYMORPHISM IN PHOSPHOHEXOSE ISOMERASE IN WHITE SHRIMP, *PENAEUS SETIFERUS* LINNAEUS, AND PINK SHRIMP, *P. DUORARUM DUORARUM**

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Abstract—1. One- and three-banded phenotypes of phosphohexose isomerase (PHI) were observed in muscle extract of white shrimp (*Penaeus setiferus* Linnaeus) and in pink shrimp (*P. duorarum duorarum*) on starch gel zymograms.

2. Based on genetic criteria, the five anodal PHI phenotypes observed on the white shrimp and pink shrimp zymograms were assumed to be under the control of four allelic genes.

3. There were no signficant differences in PHI phenotype distributions either between sexes or among samples of white shrimp from Calcasieu Lake, LA or Biloxi Bay, MS, or between sexes of pink shrimp from Tampa Bay, FL.

4. Based upon zymogram comparisons of white and pink shrimp we concluded that the migration rates of the white and pink shrimp alleles are similar.

INTRODUCTION

Electrophoretic variants of the enzyme phosphoglucomutase (PGM) have been described in brown shrimp, *Penaeus aztecus aztecus* (Proctor *et al.*, 1974) from the northern Gulf of Mexico, and in white shrimp, *P. setiferus* (Marvin & Caillouet, 1976) from the northern Gulf of Mexico and east coast of Florida. No subpopulation differences were detected within either species. In this paper we describe a polymorphism of phosphohexose isomerase in white and pink shrimp from bays in the northern Gulf of Mexico.

METHODS

We obtained white shrimp from Calcasieu Lake, LA, and from Biloxi Bay, MS, and pink shrimp from Tampa Bay, FL. All specimens were placed on dry ice as soon as possible after capture and were shipped on dry ice to the laboratory for analysis. A saline extract of abdominal muscle tissue from each shrimp was prepared according to methods used by Proctor *et al.* (1974) and Marvin & Caillouet (1976). Extracts were drawn into small pieces of Whatman No. 1 filter paper that were placed immediately in starch gel. The PHI bands resolved clearly in gels composed of 25% Sigma† and 75% Electro-starch starches. The gels continued 12.5% starch in a pH 8.0 buffer prepared by mixing one part of electrode buffer (0.06 M lithium hydroxide and 0.3 M boric acid) with 99 parts of gel buffer (0.03 M Tris and 0.005 M citric acid) (Ridgway *et al.*, 1970).

The PHI stain, a modification (F. M. Utter, personal communication) of the PGM stain described by Johnson *et al.* (1972) consisted of: 20 mg fructose-6 phosphate, 1.25 ml of 1.0 M magnesium chloride, 12.5 mg triphosphoryridine nucleotide, 12.5 mg nitro blue tetrazolium, 25 mg phenazine methosulfate, 25 units of glucose-6-phosphate dehydrogenase, and 100 ml of Tris–citrate buffer prepared by adjusting the pH of gel buffer to 7.1.

RESULTS AND DISCUSSION

PHI resolved in a single region of the gel giving one- and three-banded phenotypes typical of the dimeric PHI variations observed in many other organisms (Avise & Kitto, 1973). Four alleles were assumed to be expressed in each species. These are represented in Fig. 1 and in Tables 1 and 2 as a, b, c, and d, and f, g, h, and i for white and pink shrimp, respectively. In the comparison of the zymogram patterns of white and pink shrimp (Fig. 1) it can be seen that the migration rates of the white and pink alleles are very similar. This may mean that these allozymes are in fact identical alleles shared by the species.

The allele frequency and phenotype distributions of the two shrimp species are included in Tables 1 and 2. The phenotype distributions are in accordance with the Hardy–Weinberg equilibrium. The distributions were independent of sex, so data for males and females were combined in Tables 1 and 2.

Based on the standard deviation of the gene frequencies of white shrimp from Biloxi Bay and Calcasieu Lake, there is no significant difference between the two populations.

A similar comparion of PGM distribution among various populations of white shrimp also failed to detect population differences (Marvin & Caillouet, 1976). In addition, extensive biometric studies (Farfante, 1969) of Atlantic and Gulf of Mexico populations of white shrimp failed to show significant morphological differences.

The fact that allele distributions are the same in several areas in not necessarily indicative of a strong

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† Use of trade names in this paper does not imply endorsement of commercial products.

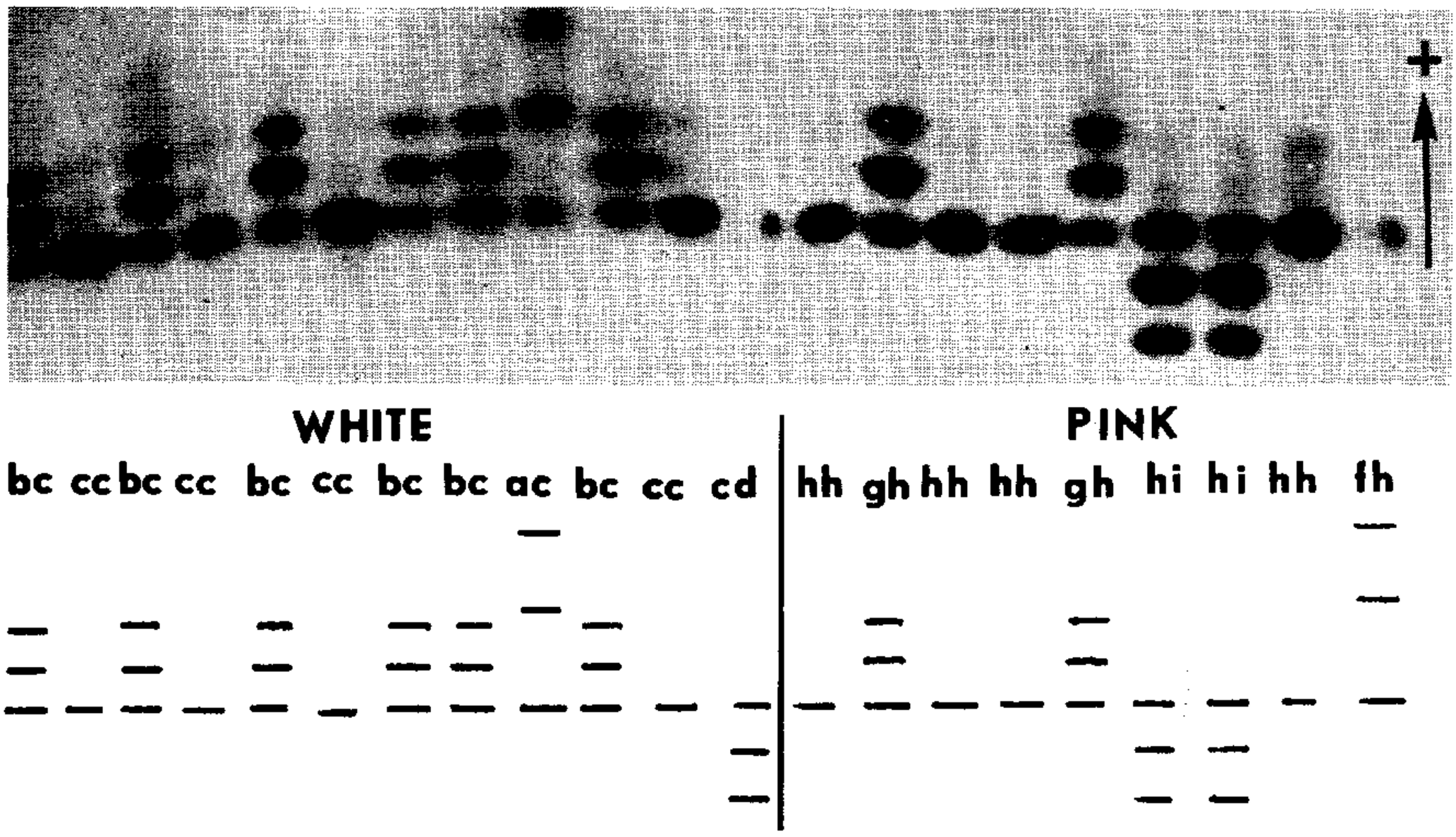

Fig. 1. Zymogram showing similarity of allele migration rates of white and pink shrimp. The d and f alleles are portrayed diagramatically only. Direction (↑) of migration toward the anode is shown.

Table 1. Distribution of PHI phenotypes, frequency of PHI alleles, and standard deviation of gene frequencies of white shrimp samples from Biloxi Bay, MS and Calcasieu Lake, LA

Location	Total length ranges mm*	Phenotypes ac	bb	bc	cc	cd	Total	Allele a	b	c	d	s† a	b	c	d
Biloxi Bay	67–130	3	4	38	110	2	157	0.0095	0.1465	0.8376	0.0064	0.005	0.020	0.021	0.004
Calcasieu Lake	72–142	2	2	42	163	2	211	0.0047	0.1090	0.8815	0.0047	0.003	0.016	0.016	0.003

* Tip of rostrum to tip of telson.
† Standard deviation of gene frequency.

$s = \sqrt{p(1-p)/2n}$

where p = gene frequency, and n = number of specimens.

Table 2. Distribution of PHI phenotypes and frequency of PHI alleles of pink shrimp from Tampa Bay, FL

Total length ranges mm*	Phenotypes fh	gh	gi	hh	hi	Total	Alleles f	g	h	i
70–172	2	10	1	175	18	206	0.0049	0.0267	0.9223	0.0461

* Tip of rostrum to tip of telson.

gene flow throughout these areas (F. M. Utter, personal communication) because small gene flow with large populations and an absence of strong selection could maintain the allele frequencies at the same levels. Conversely, selective forces could be acting to maintain gene frequencies at the same levels in the absence of interchange between two populations. Thus far, genetic sub-divisions have not been identified within the three most important commercial species of shrimp in the Gulf of Mexico.

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